

Microsatellite primers for red drum (*Sciaenops ocellatus*)

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In this note, we document polymerase-chain-reaction (PCR) primer pairs for 101 nuclear-encoded microsatellites designed and developed from a genomic library for red drum (*Sciaenops ocellatus*). Details of the genomic library construction, the sequencing of positive clones, primer design, and PCR protocols may be found in Karlsson et al. (2008). The 101 microsatellites (GENBANK Accession Numbers EU015882-EU015982) were amplified successfully and used to genotype 24 red drum obtained from Galveston Bay, Texas (Table 1). A total of 69 of the microsatellites had an uninterrupted (perfect) dinucleotide motif, and 30 had an imperfect dinucleotide motif; one microsatellite had an imperfect tetranucleotide motif, and one had an imperfect and compound motif (Table 1). Sizes of the cloned alleles ranged from 84 to 252 base pairs. A 'blast' search of the GENBANK database indicated that all of the primers and the cloned alleles were unique (i.e., not duplicated).

Summary genotypic data, based on 22–24 assayed red drum, also are given in Table 1 and include number (and size range) of alleles detected, observed and expected heterozygosity, and probability values from tests for conformity to Hardy-Weinberg equilibrium expectations. One microsatellite (*Soc734*) was monomor-

phic; the number of alleles detected at the remaining 100 (polymorphic) microsatellites ranged from 2 to 26. Estimates of observed and expected heterozygosity and tests for conformity to Hardy-Weinberg and genotypic equilibrium expectations were performed with GENEPOP (Raymond and Rousset, 1995). Observed heterozygosity (polymorphic microsatellites) ranged from 0.042 (*Soc706*) to 1.000 (11 microsatellites, Table 1) and averaged (\pm standard deviation [SD]) 0.775 ± 0.211 ; expected heterozygosity ranged from 0.042 (*Soc706*) to 0.971 (*Soc636*) and averaged 0.806 ± 0.201 . After Bonferroni correction (Rice, 1989), genotypes at 99 of the polymorphic microsatellites did not differ significantly from Hardy-Weinberg equilibrium expectations. At one locus, *Soc706*, there were only two alleles, one of which was observed only in a heterozygote; this microsatellite was not tested for Hardy-Weinberg equilibrium. Analysis with MICROCHECKER (Van Oosterhout et al., 2004) indicated the possible occurrence of null alleles at nine of the microsatellites, and single base-pair shifts (i.e., alleles differing by only a single base pair) were observed at five of the microsatellites (Table 1). Tests of genotypic disequilibrium were nonsignificant after Bonferroni correction. Given that red drum pos-

sess 24 haploid chromosomes (Gold et al., 1988), several of the microsatellites undoubtedly are linked; determination of linkage will await formal mapping studies.

Along with PCR primers for red drum microsatellites developed previously by O'Malley et al. (2003), Saillant et al. (2004), and Karlsson et al. (2008), the primers developed here will be useful in a variety of applications (Liu and Cordes, 2004), including analysis of stock structure, monitoring and assessment of red drum stock enhancement, parentage analysis as employed in aquaculture, and the generation of a genetic map for red drum. A table of the 269 PCR primers developed for red drum may be found at <<http://wfsc.tamu.edu/doc>> under the file name "PCR primers for red drum (*Sciaenops ocellatus*) microsatellites."

Acknowledgments

We thank C. Abbey for technical assistance with the Q-BOT (GENETIX), E. Saillant for assistance in the laboratory and helpful comments on a draft of the paper, and R. Vega for encouragement and support. Work was supported by the Coastal Conservation Association and Central Power and Light (CCA/CPL) Marine Development Center of the Texas Parks and Wildlife Department, the Coastal Conservation Association—Texas, and the Texas Agricultural Experiment Station (Project H-6703). This note is number 64 in the series "Genetic studies in marine fishes" and contribution no. 155 from the Center for Biosystematics and Biodiversity at Texas A&M University.

Manuscript submitted 10 June 2008.
Manuscript accepted 12 June 2008.
Fish. Bull. 106:476–482 (2008).

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Table 1

Summary data for 101 microsatellites developed for red drum (*Sciaenops ocellatus*). Primer sequences are forward (top) and reverse (bottom) primers used in PCR amplification of both DNA strands. Repeat sequence indicates repeat motif; subscript indicates number of replicates in the cloned allele. Cloned allele size (in base pairs) of the sequence in GenBank. N is the number of individuals assayed; N_A is the number of alleles detected. Size range refers to size (in base pairs) of alleles thus far detected and size includes the 21 base pair 5' tail-sequence primer used for PCR amplification. H_O/H_E is observed and expected heterozygosities, respectively. P_{HW} represents the probability of deviation from Hardy-Weinberg expectations.

Micro-satellite	Primer sequence (5'-3')	Repeat sequence	Cloned allele	N	N_A	Size range	H_O/H_E	P_{HW}
Soc628	GCACTGCTGTACTGACAC TCCAACCTCACTCGTTGTTACAG	(GA) ₂₉	181	24	18	174–220	0.917/0.932	0.783
Soc630	CGCTGCTTCTCACGCTCTG GGTGTCATGTATGGATACTGCTCTT	(CA) ₁₆	144	24	10	155–175	0.833/0.841	0.357
Soc631	TGGTCCCTCCAGCTCTGATA TCTGTTCCATGTGTGTCA	(CA) ₁₀ (N) ₂₂ (CA) ₁₄	222	24	22	189–241	1.000/0.965	1.000
Soc632	TCTTTTCTCTGCGTTTGATAG TCTCTGTGTTTTCGCTTCCA	(CA) ₁₂	242	24	2	262–264	0.083/0.082	1.000
Soc633	CAAAATGACAAGGAAGACAAGAGC CCGCCCTCAGTTACAGGAAATG	(GA) ₁₈ (N) ₂ (GA) ₅	188	24	8	191–217	0.875/0.830	0.277
Soc635	CATCAGCACGGTTATTTCTTG CCCTCTCTTTTCTCCCTCG	(CA) ₂₃	245	24	10	249–269	0.708/0.781	0.609
Soc636	AACACGTAACAACATCCATG GATCAAAATAGCATCAGTAATGT	(CA) ₃₅	150	23	25	131–217	0.957/0.971	0.134
Soc637 ¹	AGAGGTTAGAAAGGGAGAA AGTATCAAAAACCTGGCATCC	(CA) ₃₁	194	22	20	178–230	0.818/0.940	0.007
Soc638	CTTTCATTTGGACTGGCTTTG TGGTCTGCTCTGCTTTTGAT	(GA) ₁₄	220	24	5	236–250	0.792/0.755	0.323
Soc639	ATCTTCTCTCACAAACACTCAC CCAAAACCTGCAAGGATGTC	(CA) ₁₃	138	24	7	148–168	0.792/0.740	0.989
Soc640	AGGACATTTGGAGTGGAAAGAGTA ATGGGGACAGGAGGTTTTCTA	(CA) ₁₄	159	24	13	179–209	0.875/0.898	0.225
Soc641	ATGCGGAGTAGAGAGGAGG TGACCTGAATGAAGATGTATGGA	(CA) ₁₇ (N) ₂ (CA) ₆	136	23	20	142–202	0.913/0.958	0.117
Soc642	CAGAGAAGTTACAGGAGGTG ATGTGCTGGGACAGGTTG	(CA) ₂₂	200	23	9	210–228	0.870/0.881	0.539
Soc644	GCTACGGTCGGGAATCAGA GCTGCCCTTCAGTGGTTTT	(CA) ₃₂	167	23	18	155–205	0.913/0.952	0.319
Soc645 ¹	GAGTTGGTCAATAGCCACAGG ATCTGAAAGGCGAGGTGTTG	(CA) ₂₀	150	24	10	157–181	0.708/0.891	0.025
Soc646	GGGAAAGTAGATAGGGGCACA AGAGGTCAGGGTTGAGCAGAGT	(CA) ₁₆	132	22	4	130–156	0.273/0.318	0.559
Soc647	GCACAGATTCGTCCCAGATT TGTTCAGTTGCTCACAAACCA	(CA) ₅₁	247	23	26	203–283	0.957/0.967	0.463

continued

Table 1 (continued)

Micro-satellite	Primer sequence (5'-3')	Repeat sequence	Cloned allele	N	N _A	Size range	H _O /H _E	P _{HW}
Soc648	GTTCCAGATGGGATGTAAC GCTACTGCCACCACAAACAC	(CA) ₅ (N) ₂ (CA) ₂₂	181	24	14	179-225	0.833/0.888	0.266
Soc649 ¹	GTACTTGTAGTAATCAGGTAATTT AAACGCACCTCTTTGAGACTA	(TG) ₂₀	154	24	11	152-182	0.708/0.878	0.040
Soc650 ¹	CCGTGTTTGGCTTT CAATGTATGGGTATGGGTAGG	(CA) ₂₂	125	24	14	127-175	0.583/0.893	0.002
Soc651	TGAAAGACGAAATTCAGCAAAA AGGAAGCAGTGGATAGTAAA	(CA) ₂₃	187	24	20	193-263	1.000/0.931	1.000
Soc652	TCGCCATCATTAATAACT GTTCTCAAAAAGAGTCTACCTGTC	(CA) ₁₉	196	24	10	204-232	0.833/0.785	0.821
Soc653 ^{1,2}	GAAACAGCTCCACACAG TCCTCCCTTCGGCTCATCA	(CA) ₂₆	252	24	17	138-274	0.792/0.931	0.157
Soc654 ²	CTCCGCTGCCAAACTGAC TGTGCTCTACATCCTCCTCCT	(CA) ₁₃	164	23	5	173-186	0.565/0.575	0.191
Soc655	CTGAAAGGCGGTTGGTTT GAGGATGCAGAGTCAAGCAAGA	(CA) ₁₈ (N) ₂ (CA) ₃ (N) ₂ (CA) ₈	166	24	10	172-192	0.792/0.836	0.642
Soc656	CGTGTGAGACAGGTGGTAGT GTAGGCGTGGAGACGGAGT	(CA) ₂₄	213	24	23	221-279	1/0.955	0.442
Soc657	GGAAAGCAAAGCAAAGAAACT AGCCGAATGAGACAGAGGAAA	(CA) ₃₄	232	22	17	210-268	0.955/0.946	0.757
Soc658	AATCTCCAGTGCCTTTGA CTGCTTTTCCCTCTAATTTCTC	(GA) ₁₄	149	24	7	162-176	0.542/0.558	0.789
Soc659	GCATCCCTCCCTCTCTCC GCCTGGCAAACATCCAACCTT	(CA) ₁₇ (CA) ₁₂ (N) ₂ (CA) ₂ (N) ₂ (CA) ₅	189	23	10	200-228	0.870/0.854	0.462
Soc660 ²	TTGCCAATGTTCTTTCTCTCT ATTCCTACTCTGCGCAAGAT	(N) ₂ (CA) ₂ (N) ₂ (CA) ₇	123	24	11	130-184	0.833/0.847	0.783
Soc661 ¹	ACCGCCTCAAAACAACACA AGGAGATTGGGAGTGGAGATA	(CA) ₁₃	145	24	11	154-176	0.667/0.859	0.004
Soc662	CGTCTTTAGGAAGTGTGGC CCTGTCTGGAGGGGAAAAC	(CA) ₂₀ (N) ₂ (CA) ₆ (N) ₂ (CA) ₃	108	22	13	90-144	0.818/0.910	0.385
Soc663	TCAGGGTATGTACGCAGATG CAAGCACTTCACGAGGAAC	(CA) ₁₄	172	24	21	190-274	0.917/0.930	0.753
Soc664	GAGGTTCAAGTTGGCTGCTG CGTGTGTGTTTCGCTCAGTT	(CA) ₂₃	136	24	15	137-169	0.875/0.907	0.268
Soc665	TCACAGTGGCTCTCCAGGTAA TTGCCCTCTTGTCTGTTCAFTCT	(GA) ₃₃	132	24	22	115-189	0.833/0.944	0.268
Soc666 ¹	TAATCTGTGTCTCCAGGTG GACGCAAGGCTGAGGCATA	(CA) ₄ (N) ₂ (CA) ₂₁	201	24	18	207-263	0.750/0.921	0.020

continued

Table 1 (continued)

Micro-satellite	Primer sequence (5'-3')	Repeat sequence	Cloned allele	N	N _A	Size range	H _O /H _E	P _{HW}
Soc667	TAAAGCTCTGTCCATCACTG CATCTACGAAATGCCCAACA	(CA) ₁₄ (N) ₄ (CA) ₁₅	232	23	6	245–261	0.652/0.699	0.198
Soc668	TGATGAGGACCAAGTGACAAC ATCAGTGTTTTTCATTAGCC	(CA) ₁₈	96	23	15	107–163	0.870/0.901	0.095
Soc669	GAAGGAGGCAGGCACACATA GAGAGCGAGCGAGAGAAAAGA	(CA) ₄ (N) ₂ (CA) ₂₁	117	23	17	115–167	0.957/0.889	0.996
Soc670	TTCTGCCCGTCACAGCAC CAAAGAGAGATGAATAACCCAAAG	(CA) ₃₀	245	23	12	225–273	0.826/0.852	0.296
Soc671	CGCCTCTCTTCCCTCAGATGT ACAGTGGGCAATCCATACA	(CA) ₃₀ (N) ₄ (CA) ₄	228	23	14	233–271	0.826/0.910	0.152
Soc672	CGTATGGTGAGTGTGGCA TGTCGTCTCTGAATGTCTCT	(CA) ₂₂	199	24	19	199–243	0.875/0.946	0.056
Soc673	AAAGACTGACACAAGCTGACA AATCTCTGCTCAITTCCTCATCT	(CA) ₂₄ (CAGA) ₄ (N) ₄ (CAGA) ₂ (N)	194	22	10	193–227	0.773/0.819	0.807
Soc675 ¹	TGTCCCCATAAAGAACAAGG ACACAACGCTACAGGAAGGC	(CAGA) ₂	96	24	6	108–234	0.417/0.608	0.037
Soc676	TGAACGTGACGTCCTGTCAT CCTTGTCTTTATGGGGACA	(CA) ₂₀	166	24	15	173–211	0.875/0.919	0.320
Soc678	CTGGCTGGTTGATGTAAGTC AGACAGTGGGGGTTAGAT	(CA) ₁₉	128	24	12	132–158	0.875/0.898	0.577
Soc679	ACACCTTCCACTGACTGACCAC GAATGTGGGTGCTGGGT	(CA) ₂₇	146	24	14	162–194	0.792/0.889	0.013
Soc680	GCTGCCCTCTCTGTCACTCT TCACGCCACCTTCTCCTCTTT	(CA) ₁₂	93	22	19	106–152	0.955/0.949	0.632
Soc681	TATGGCTCCGACACACTCCT CCACCCCAGTAGACACTCAGA	(GACA) ₄ (CA) ₁₂	111	24	9	123–151	0.875/0.849	0.671
Soc682	TCCACTGTAGGTGTTGTTTCA ACTTTTAGGGGGGAGAGTC	(CA) ₁₅	200	24	11	202–236	0.750/0.880	0.171
Soc683	TTCCACACATAGATACTAAACT AGCGTCATAATCCAACGTCA	(CA) ₆ (N) ₂ (CA) ₇ (GA) ₅ (N) ₈ (GA) ₄ (N) ₂ (GA) ₂	185	23	7	190–230	0.565/0.647	0.312
Soc684	CAGCCATACAGCGGCAC TTTGAATAGAAGTCAGAAGTGC	(N) ₂ (GA) ₆ (N) ₂ (GA) ₉	198	24	13	185–233	0.917/0.833	0.860
Soc685	TCAAACAGGTCATTTGGTGA AGGAGAAACGCAGGGAAGA	(CA) ₁₄	215	23	2	233–235	0.261/0.232	1.000
Soc686	AAAGTGACCCCTGAGTTCCTCTG GCAAAAACAATGAAAACCTCT	(CA) ₁₉	236	23	12	233–265	0.826/0.881	0.564
Soc687	GCTGGAAGGGGAGTCTTATGA AAGGCTCTCTCAAGCAGTGT	(CA) ₁₂	157	23	16	172–206	0.870/0.928	0.351

continued

Table 1 (continued)

Micro-satellite	Primer sequence (5'-3')	Repeat sequence	Cloned allele	N	N _A	Size range	H _O /H _E	P _{HW}
Soc688	GCTCTCTTGTCTCCATACCTG GGGAAACCTGCTGTGACCA	(CA) ₁₈	192	24	15	198-242	0.875/0.854	0.901
Soc689	GACTCTTCAATCCTACTACCA ACATTTCTTTTGTCCGTTCA	(CA) ₂₅	182	23	20	204-246	1.000/0.937	0.951
Soc690	CGTCTTCTGTGTTGTGGGA TGATTCATCTGCGTCTGTT	(GA) ₂₁	101	22	11	109-139	0.909/0.862	0.100
Soc691	CAGTGAGAGACGCAAAACCAG GTCAAGTAGGTAATAAAGCCTGA	(CA) ₃₁	129	22	15	112-158	0.909/0.926	0.832
Soc692	TGCTGCCATTGAGAAGAGA TTTGTATGTTAGGGGTTGTGT	(CA) ₁₀	117	23	6	126-140	0.652/0.647	0.650
Soc693	AAGTTGTTTCTTTTGTCCAGTA TAGATGAAGGCTTGTTTTCTCT	(GA) ₁₈ (N) ₁ (GA) ₇	192	24	22	279-337	1.000/0.950	0.022
Soc694	CTCGCTCCCATCGTGACT TCCTGAAAGTTGTGTTGTCC	(CA) ₁₁	168	21	9	185-207	0.810/0.846	0.424
Soc695	TCTGGAGGGATGATGTGTTT CCTGTTTCACTGCTACTCGC	(CA) ₂₁ (N) ₂ (CA) ₅	135	23	16	129-187	0.957/0.912	0.780
Soc696	GAAAATGGTGAAAACCCTGA CAAAATGGAGAAGCCTGAAG	(CA) ₃₁	207	23	21	191-253	1.000/0.954	0.937
Soc697	AAGCACGCAATCTATGAAACAC TGTGGGAAAACATCCAGAG	(CA) ₁₀	166	22	7	183-199	0.682/0.744	0.421
Soc698	TCTCAAATCTTCCAATCAGCAG CGACAGGGAGTGACCAACAG	(CA) ₁₁	133	22	9	152-172	0.818/0.819	0.684
Soc699	AGCCAGCAACTGAATACCA CAAAGCCACCTCCTGATTT	(CA) ₁₃	163	23	15	170-224	0.783/0.853	0.218
Soc700	GCTGAACCTGTGAGGCAGATGA CGTAAATAAGGAAACAAACAAGA	(CA) ₂₈	245	22	22	249-305	0.955/0.946	0.701
Soc701	ATCCAGGTTTAGAGGCTGTCA TTCAGGAAAAGTCCACACAGA	(CA) ₆ (N) ₂ (CA) ₁₅	120	23	12	129-169	0.739/0.846	0.034
Soc703	TCTCCGTGTAAGATGATGGTC GAGGGGAAACAACACTGCTAA	(CA) ₁₈	235	23	16	236-278	0.913/0.923	0.910
Soc704	CCCAGCGTTTCCCCTAAT ACATCCCCCTCTGTTCTCTCT	(GA) ₁₅	237	22	12	254-302	0.682/0.722	0.303
Soc705 ²	CTGCCTGGATTGCCTTTTAG TTCCTGCTGTTGAGGACGATG	(CA) ₇ (N) ₂₈ (CA) ₄	215	23	9	235-246	0.826/0.752	0.755
Soc706	ACTCTGTTGCTCCACTACCCA GCTCTTCTCCTGTTTGTGTTGA	(CA) ₅ (N) ₂ (CA) ₈	150	24	2	170-176	0.042/0.042	na
Soc707	TTCCTCTCTTCACTCCTGTT CAACACTGCCTCCCTATGG	(CA) ₂₁	156	23	18	173-217	0.870/0.932	0.287

continued

Table 1 (continued)

Micro-satellite	Primer sequence (5'-3')	Repeat sequence	Cloned allele	N	N _A	Size range	H _O /H _E	P _{HW}
Soc708	TTCCCCTAGAGCTGTGATTGA TCTGACTTCCCTCGCCCAFT	(CA) ₁₇	130	23	9	139–157	0.870/0.878	0.258
Soc709	CTGATGAATGGACTGAACAC TGTGAGAGGAACAGAGACG	(CA) ₂₂	200	22	7	201–221	0.682/0.740	0.261
Soc710	TGTTGTAGTGAAGGCAAACC TGGCAGGGAGAAATAGAGAA	(CA) ₁₈ (N) ₂ (CA) ₄	102	22	10	107–131	0.591/0.674	0.033
Soc711	CCTCCCCACCCTCTCTGTG AGTCGCTGCTGTGTGTGT	(CA) ₅ (N) ₂ (CA) ₁₄	244	23	10	262–288	0.783/0.807	0.552
Soc712	CAGCAGAGGGCAAAAATGA AGGGTGGGTGGTGTGTCA	(GA) ₁₄	84	23	7	95–111	0.652/0.557	0.836
Soc713	AATAGTTTCCCTCGGATTGACG TGGCTTAGACAAGTGGTGCT	(CA) ₁₈	189	24	11	189–211	1.000/0.888	0.919
Soc715	TTTTCCCCTCTTTCCACAG GCAACACAGTCAGCCACA	(CA) ₁₀	98	24	4	114–124	0.583/0.666	0.716
Soc716 ²	ATGTTGTTTGGCTTGTGAG AGAGCGGCAGTCATCTGTTC	(CA) ₁₀ (N) ₂ (CA) ₆	144	24	15	146–186	0.833/0.921	0.040
Soc717	ACGGCAACTGGGGTCAAC TTCCATCGTGTAGTCAACAAC	(CA) ₆ (N) ₂ (CA) ₅	241	22	3	260–264	0.636/0.609	0.818
Soc718	CCCTCTGTTTTCTCTGGGATTT CTTTGGTGTGTGGTGTGTCT	(CA) ₁₆	190	23	9	203–223	0.783/0.796	0.041
Soc719	CACCTTCTACTCCCATCA CCTCCTTCTTGGCTTCAFA	(CA) ₂₇	183	24	17	190–230	1.000/0.917	0.397
Soc721	GGTAAAGTGTAAAATGCCAATAG AGGAAACGAAAAGAGGAAA	(CA) ₁₀ (N) ₂₄ (CA) ₁₂	203	23	10	209–229	0.783/0.847	0.142
Soc723	CAGATGGCACTAAGGAGA CAGATAAGTAGAGGTGGAAGACA	(CA) ₇ (N) ₂ (CA) ₂₄	170	24	19	183–245	0.833/0.940	0.171
Soc724	GTATTTTGAGCCTGCGTTGTA CATGAACCCGTCATTTGC	(CA) ₂₂	194	24	11	198–234	0.833/0.892	0.021
Soc725	GAAGCGAAAATAAGGCTGA GTTTAGTTTGGTCTGTTCAATC	(CA) ₁₅ (CA) ₁₅ (N) ₂ (CA) ₄	88	22	9	101–123	0.773/0.841	0.088
Soc726	GCTTCTATTGATCTGCGTGTG CAAGTGGGGAGGAGAGACA	(N) ₂ (CA) ₁₁	146	24	16	140–184	0.958/0.918	0.270
Soc727 ¹	AGGCATCATTTACAGGCTCA AACCAACACACGAGGCTGA	(CA) ₁₇	138	22	8	136–164	0.591/0.779	0.071
Soc729	CTTCTTCCACCTGTAACCTGAATC CTTTGTCTCCGCTTGTGTTTC	(CA) ₉ (N) ₂ (CA) ₄	137	23	13	156–184	0.913/0.930	0.810
Soc730	GCACAGGGAGATAAACACAG CTGAAGAAAAGCCAGAGTGAA	(CA) ₁₄	92	24	4	109–115	0.333/0.487	0.019

continued

Table 1 (continued)

Micro-satellite	Primer sequence (5'-3')	Repeat sequence	Cloned allele	N	N _A	Size range	H _O /H _E	P _{HW}
Soc731	CAACCGATGAGAGCAGAGACT TGTGTGTAGGTGAGACAAAAGAA	(CA) ₂₂	224	23	9	220-254	0.391/0.484	0.133
Soc733	GCTGATGATGAACTGGTGCT TTTCTTGTATGCTCTGTTTGC	(CA) ₁₂	158	23	3	176-188	0.130/0.127	1.000
Soc734	CAGATTGGAACTGACACACAC AAGCCCTTCTTGGAGATT	(CA) ₁₀ (N) ₂ (CA) ₃	90	22	1	109	0/0	—
Soc735	CCATCAGGAGGCTTTTGTCA AAGAAGTAGGGTCAGCACACTGT	(CA) ₃₁	187	23	23	164-244	1.000/0.965	1.000
Soc736	GAACCCACTGCGAAACT GCCTACAGATTGAGAACCACT	(CA) ₃ (N) ₂ (CA) ₉ (N) ₂ (CA) ₆	168	22	3	188-196	0.136/0.132	1.000
Soc737	TCCAGGAAGTGGTCGGTTT GGGAGAAATGTGTGAATGCTTG	(CA) ₆ (N) ₂ (CA) ₁₉	197	22	12	203-247	0.818/0.869	0.242
Soc738	TGTAACAGACAGACTGAAGC CTGGGTGAAAGGCAGAGTA	(CA) ₂₈	117	23	21	116-170	1.000/0.949	0.651
Soc739	TTGTGTTTTTCCCTCTGCTG TGTGTTTATGTTGGTGGTG	(CA) ₃ (N) ₂ (CA) ₃ (N) ₂ (CA) ₁₀	188	23	16	201-251	1.000/0.938	0.894

¹ Microsatellites where occurrence of null alleles was indicated by analysis with MICRO-CHECKER

² Microsatellites with observed alleles differing by only a single base

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